

Gencore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2001, 16:18:27 ; Search time 64.32 Seconds
(without alignments)

10.632 Million cell updates/sec

Title: US-09-331-631a-37
Perfect score: 52

Sequence: 1 CXXXCXXXXXXCXXXC 20

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_36:*

1: /SIDS1/gcadata/geneseq/geneseq/AA1980.DAT:*

2: /SIDS1/gcadata/geneseq/geneseq/AA1981.DAT:*

3: /SIDS1/gcadata/geneseq/geneseq/AA1982.DAT:*

4: /SIDS1/gcadata/geneseq/geneseq/AA1983.DAT:*

5: /SIDS1/gcadata/geneseq/geneseq/AA1984.DAT:*

6: /SIDS1/gcadata/geneseq/geneseq/AA1985.DAT:*

7: /SIDS1/gcadata/geneseq/geneseq/AA1986.DAT:*

8: /SIDS1/gcadata/geneseq/geneseq/AA1987.DAT:*

9: /SIDS1/gcadata/geneseq/geneseq/AA1988.DAT:*

10: /SIDS1/gcadata/geneseq/geneseq/AA1989.DAT:*

11: /SIDS1/gcadata/geneseq/geneseq/AA1990.DAT:*

12: /SIDS1/gcadata/geneseq/geneseq/AA1991.DAT:*

13: /SIDS1/gcadata/geneseq/geneseq/AA1992.DAT:*

14: /SIDS1/gcadata/geneseq/geneseq/AA1993.DAT:*

15: /SIDS1/gcadata/geneseq/geneseq/AA1994.DAT:*

16: /SIDS1/gcadata/geneseq/geneseq/AA1995.DAT:*

17: /SIDS1/gcadata/geneseq/geneseq/AA1996.DAT:*

18: /SIDS1/gcadata/geneseq/geneseq/AA1997.DAT:*

19: /SIDS1/gcadata/geneseq/geneseq/AA1998.DAT:*

20: /SIDS1/gcadata/geneseq/geneseq/AA1999.DAT:*

21: /SIDS1/gcadata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	52	100.0	31	21	Wnt antagonist protein Nucleotide used in Pyruaria pubera t Leech derived frags Leech derived frags Leech derived frags Hirudinase. Hirud Amino acid sequenc Elastase inhibit Guamein, an elast Sequence of human Human metallothionein
2	52	100.0	44	17	R88208
3	52	100.0	48	18	W05616
4	52	100.0	50	17	R86122
5	52	100.0	50	17	R86123
6	52	100.0	51	17	R96121
7	52	100.0	55	16	R79209
8	52	100.0	55	19	W46918
9	52	100.0	57	17	W03663
10	52	100.0	57	19	W0929
11	52	100.0	60	14	R40209
12	52	100.0	60	21	Y62332
13	52	100.0	61	19	W61601
14	52	100.0	61	20	W87595
15	52	100.0	61	21	Y82331
16	52	100.0	61	21	Y57822
17	52	100.0	62	21	Y57810
18	52	100.0	63	21	Y57811
19	52	100.0	68	12	R4774
20	52	100.0	68	13	R25720
21	52	100.0	68	15	R53383
22	52	100.0	70	21	Y75953
23	52	100.0	73	20	Y59335
24	52	100.0	84	20	W87597
25	52	100.0	84	20	W87598
26	52	100.0	84	20	W87600
27	52	100.0	103	20	Y77949
28	52	100.0	105	20	W87700
29	52	100.0	105	21	Y72329
30	52	100.0	107	21	W87451
31	52	100.0	108	20	Y35998
32	52	100.0	108	20	W87710
33	52	100.0	108	21	Y22320
34	52	100.0	108	21	Y77408
35	52	100.0	108	21	Y77409
36	52	100.0	108	21	Y23332
37	52	100.0	109	17	R84086
38	52	100.0	109	20	Y12933
39	52	100.0	109	21	Y22327
40	52	100.0	111	20	W87704
41	52	100.0	111	20	W87705
42	52	100.0	111	20	W87709
43	52	100.0	111	21	Y68910
44	52	100.0	111	21	Y67266
45	52	100.0	111	21	Y32328

ALIGNMENTS

RESULT	1
ID	Y70731 standard; protein; 31 AA.
XX	
AC	V70731;
XX	
DT	24-JUL-2000 (first entry)
XX	
DE	Wnt antagonist protein consensus sequence-1.
XX	
KW	Wnt antagonist; contraceptive; contraceptive vaccine; oocyte development; female primate contraception; oocyte viability.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Misc-difference 2
FT	Location/Qualifiers
FT	/label= Unknown
FT	/note= "Xaa may be 9 amino acids in length; some amino acids may be absent"
FT	Misc-difference 4
FT	/label= Unknown
FT	/note= "Xaa may be 42 amino acids in length; some amino acids may be absent"
FT	Misc-difference 14
FT	/label= Unknown
FT	Misc-difference 15
FT	/label= Unknown
FT	Misc-difference 16
FT	/label= Unknown
FT	Misc-difference 17
FT	/label= Unknown
FT	Misc-difference 18
FT	/label= Unknown
FT	Misc-difference 19

CC also have an antibiotic effect. The fahsin family of proteins comprise 50/51 amino acids and occur in various isoforms. These peptides are useful in the treatment of diabetes mellitus, blood clotting disorders, CC disorders of neutrophil function, e.g. emphysema, rheumatoid arthritis, CC HIV infection and other immunological and inflammatory diseases.

SQ Sequence 50 AA;

Query Match 100.0%; Score 52; DB 17; Length 50;
Best Local Similarity 20.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXXCXXXXXXXXXXXXC 20
|:|:|:|:|:|:|:|:|:|:|:|:
Db 27 crialcpngfadvdengcelpc 46
|:|:|:|:|:|:|:|:|:|:|:
27 criyccpkgfevdengcelpc 46

RESULT 6 R96121

ID R96121 standard; Peptide; 51 AA.
XX
AC R96121;
XX

DT 17-DEC-1996 (first entry)
DE Leech derived fahsin based protease inhibitor #1.

KW Protease inhibitor; isoform; elastase; chymotrypsin; trypsin; leech; tissue; secretion; saliva; fahsin; antibiotic; diabetes mellitus; blood clotting disorder; neutrophil function; emphysema; rheumatoid arthritis; HIV infection; human immunodeficiency virus.

OS Limnatis nilotica.

PN W09613585.A1.

XX 09-MAY-1996.

XX DE 27-OCT-1995; 95WO-EP04223.

XX PR 14-MAR-1995; 95EP-0103437.

XX PR 28-OCT-1994; 94EP-0117053.

XX -PA (CLOD-) CLODICA SA.

PI Voerman G;

XX DR WPI; 1996 239498/24.

PT New protease inhibitors from the leech *Limnatis nilotica* - for treating, e.g. blood clotting disorders, HIV infection, diabetes mellitus etc.

XX PS Claim 3; Page 26; 41pp; English.

XX The protease inhibitor peptide isoforms given in R96121-23 are elastase/chymotrypsin- and trypsin inhibitors which may be isolated from leech tissue or leech saliva. These peptides belong to the family of leech derived substances named fahsin's which also have an antibiotic effect. The fahsin family of proteins comprise 50/51 amino acids and occur in various isoforms. These peptides are useful in the treatment of diabetes mellitus, blood clotting disorders, disorders of neutrophil function, e.g. emphysema, rheumatoid arthritis, HIV infection and other immunological and inflammatory diseases.

XX SQ Sequence 51 AA;

Qy 1 CXXXXCXXXXXXXXXXXXC 20
|:|:|:|:|:|:|:|:|:|:|:
Db 27 crialcpngfadvdengcelpc 46
|:|:|:|:|:|:|:|:|:|:
27 criyccpkgfevdengcelpc 46

RESULT 7 R79020

ID R79020 standard; protein; 55 AA.
XX
AC R79020;
XX

DT 09-MAR-1996 (first entry)

DE Hirustasin.

KW Hirustasin; serine protease-inhibitor; anticoagulant; antimetastatic; prophylactic.

OS Hirudo medicinalis.

XX FH Key Location/Qualifiers
FT Protein 1..55
FT /label= hirustasin

XX PN EP662514-A1.

XX PD 12-JUL-1995.

XX PR 23-DEC-1994; 94EP-0810750.

XX PR 07-JAN-1994; 94EP-0810006.

XX PA (CIBA) CIBA GETTY AG.

PA (UCPG-) UCP GEN-PHARMA AG.

XX PT Fritz H, Heim J, Sommerhoff C;

XX DR WPI; 1995-242017/32-5.

XX DR N-PSDB; Q97593, Q97594.

XX PT New serine protease inhibitor, hirustatin, from leech - also related DNA and vectors, is useful as an anticoagulant for treating e.g. thrombosis.

XX PS Claim 1; Page 18; 36pp; English.

XX Hirustatin can be isolated from medical leeches, synthesized chemically or prepared by recombinant DNA techniques, i.e. gene cloning in 2 micron plasmid DNA and expression in host cells, especially *S. cerevisiae*. Hirustatin is used in the treatment of conditions associated with chymotrypsin, tissue kallikrein or cathepsin-G. It is also used as an antimetastatic and as an anticoagulant for treatment/prevention of thrombosis, embolism, etc., and in the treatment of hypertension.

XX SQ Sequence 55 AA;

Query Match 100.0%; Score 52; DB 16; Length 55;
Best Local Similarity 20.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXXCXXXXXXXXXXXXC 20
|:|:|:|:|:|:|:|:|:|:
Db 29 criickyglkkdengcepc 48

RESULT 8 W46918

ID W46918 standard; protein; 55 AA.
XX
AC W46918;

Query Match 100.0%; Score 52; DB 17; Length 51;
Best Local Similarity 20.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

DT 24-JUN-1998 (first entry)
 XX
 DE Amino acid sequence of a Kallikrein inhibitor called Hirustasin.
 XX Inhibitor; tissue Kallikrein; Hirustasin; crystalline;
 KW Kallikrein/kinin system; X-ray structure; inhibition;
 KW complex formation; leech.
 XX OS Hirudo medicinalis.
 XX PN WO9803537-A2.
 XX PD 29-JAN-1998.
 XX PF 23-JUL-1997; 97WO-EP03990.
 XX PR 24-JUL-1996; 96EP-0810487.
 XX PA (NOVOS) NOVARTIS AG.
 PI Di Marco S, Grutter M, Mittl P;
 XX DR WPI; 1998-120691/11.
 XX PT New hirustasin and hirustasin-kallikrein crystals - used for design
 PT or identification of compounds which interfere with complex
 PT formation, useful as, e.g. serine protease inhibitors
 XX PS disclosure; Page 42; 45pp; English.
 XX CC The present sequence represents an inhibitor of tissue Kallikrein called
 CC Hirustasin. The crystalline form of the protein is claimed. Hirustasin
 CC may have a potential medical application in those diseases where tissue
 X-ray structure of the Hirustasin/Kallikrein system seems to play a major role. Coordinates for the
 CC resolution are given in the specification. The Hirustasin/Kallikrein
 CC crystal structure can be used for the design or identification of the
 CC structure of compounds that can interfere with the building of the
 CC Hirustasin/Kallikrein complex. It can also be used to design new
 CC inhibitors of serine proteases such as Kallikrein.
 XX SQ Sequence 55 AA;
 Query Match 100.0%; Score 52; DB 19; Length 55;
 Best Local Similarity 20.0%; Pred. No. 1 8e+02;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CAXXCAXXXXXXCXXC 20
 Db |::|::|::|::|::|::|:
 29 circkyqikkengceypc 48
 RESULT 10
 ID W50928
 XX ID W50928 standard; protein; 57 AA.
 AC W50928;
 XX DT 31-JUL-1998 (first entry)
 DE Guamerin, an elastase-inhibiting protein isolated from Korean leech.
 DE Guamerin; Korean leech; elastase inhibition; subtilisin;
 KW protease inhibitor.
 XX OS Hirudo nipponia.
 XX PN WO9803663-A1.
 XX ID W03663 standard; protein; 57 AA.
 AC W03663;
 XX DT 18-JUN-1997 (first entry)
 DE Elastase inhibiting protein from the leech Hirudo nipponia.
 XX Elastase inhibitor; rheumatoid arthritis; emphysema; psoriasis;
 KW guamerin; Korean leech; Hirudo nipponia; over-production; excess.
 XX OS Hirudo nipponia.
 XX PN GR2300190-A.
 XX PD 30-OCT-1996.
 XX PF 07-SEP-1995; 95GB-0018312.
 XX PR 27-APR-1995; 95KR-0010206.
 XX PA (KOAD) KOREN ADV INST SCI & TECHNOLOGY.
 PA (KANK-) KANKOKU KAGAKU GIJUTSUIN.
 XX PI Hong S, Jung H, Kang K, Kim D, Lee J;
 DR WPI; 1996-467114/47.
 XX PT New specific elastase inhibitor from the leech Hirudo nipponia -
 PT useful for treatment of rheumatoid arthritis, emphysema and
 PT psoriasis.
 XX PS Claim 1; Page 14; 23pp; English.
 XX CC W03663 represents the sequence of an elastase-inhibiting protein
 CC designated Guamerin. The protein was derived from the guamerin (Korean
 CC leech Hirudo nipponia), it is used to treat diseases related to
 CC excessive elastase production, especially rheumatoid arthritis.
 CC emphysema and psoriasis. The protein specifically inhibits elastase
 CC so has fewer side effects than known elastase inhibitors. Also it has
 CC lower inhibition constant (81 fM), indicating higher activity, and
 CC relatively good stability against heat, acids and alkalis (no loss
 CC of activity after 15 mins. at 100deg.C or at pH 1-11).
 XX SQ Sequence 57 AA;
 Query Match 100.0%; Score 52; DB 17; Length 57;
 Best Local Similarity 20.0%; Pred. No. 1 9e+02;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CXXCAXXXCAXXXXXXCXXC 20
 Db |::|::|::|::|::|::|:
 35 emifcpgfkdqndqgeypc 54

XX	W09831795-A2.	DR	N-PSDB; VM3774.
XX	23-JUL-1998.	XX	New method for mass production of antimicrobial peptides - by
PD		PT	constructing fusion genes comprising acidic and antimicrobial
XX		PT	peptide genes and transforming host with vector containing these
PT	30-DEC-1997;	PT	peptide genes and transforming host with vector containing these
PR	30-DEC-1997;	PT	peptide genes and transforming host with vector containing these
XX	17-JAN-1997;	XX	Example 1; Fig 1A; 52pp; English.
PR	17-JAN-1997;	PS	
PA	(INCY-) INCYTE PHARM INC.	XX	
XX		CC	The invention relates to mass production of antimicrobial peptides. The
PT		CC	method comprises constructing a fusion gene containing a first gene
PT	Goli SK, Hillman JL;	CC	encoding a negatively charged acidic peptide having at least two cysteine
XX		CC	residues, and a second gene encoding a positively charged basic
DR	WPI: 1998-414095/35.	CC	antimicrobial peptide. A host microorganism is transformed with a vector
DR	N-PSDB; V45334.	CC	containing the fusion gene and then cultured. The expressed antimicrobial
XX		CC	peptide is then recovered. The method is used to mass produce
PT	Human metallothionein, HMBP-1 - used to develop products for	CC	antimicrobial peptides in recombinant microorganisms. The inhibitory
PT	diagnosis, prevention and treatment of heavy metal toxicity, cancer,	CC	effect of the expressed antimicrobial peptide upon the growth of the host
PT	inflammatory disease and immune disorders	CC	microorganism is considerably reduced by fusing it to the acidic peptide.
XX		CC	Therefore, the use of the fusion gene provides an economic, recombinant
PS	Claim 1; Fig 1; 53pp; English.	CC	alternative of mass producing antimicrobial peptides, which overcomes the
XX		CC	disadvantages of low-productivity and poor economy, previously
CC	The human metallothionein HMBP-1 (heavy metal binding protein),	CC	encountered by recombinant and chemical methods. The present sequence
CC	polypeptides can be used to treat heavy metal toxicity, e.g. myopathy,	CC	represents the guamerin gene product. Guamerin can be used as an acidic
CC	encephalopathy, renal nephropathy or necrosis, liver necrosis or	CC	peptide in the construction of the fusion protein.
CC	cirrhosis, anaemia, myocardial damage, and pneumonitis or any other	XX	
CC	condition or disease caused by exposure to heavy metals. They can also		
CC	be used to treat immune disorders e.g. bronchial asthma, chronic		
CC	obstructive pulmonary disease, pneumonia, multiple sclerosis, rheumatoid		
CC	arthritis, inflammatory bowel disease, chronic hepatitis, cerebral		
CC	oedema, or inflammatory disease or cancers.		
XX	Sequence 61 AA;	SQ	
Query Match	100.0%; Score 52; DB 19; Length 61;	Query Match	100.0%; Score 52; DB 20; Length 61;
Best Local Similarity	20.0%; Pred. No. 2e+02;	Best Local Similarity	20.0%; Pred. No. 2e+02;
Matches	4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;	Matches	4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
Qy	1 CXXXCXXXXXXCXXC 20	Qy	1 CXXXCXXXXXXCXXC 20
Db	29 ckksccscppvgcakcangc 48	Db	37 ceifcpngfkvdengceypc 56
RESULT	14	RESULT	15
WT7595	W87595 standard; peptide; 61 AA.	WT7595	Y82331 standard; protein; 61 AA.
XX		XX	
AC	W87595;	AC	Y82331;
XX		XX	
DT	19-MAR-1999 (first entry)	DT	22-JUN-2000 (first entry)
DE		XX	
XX		DE	Human metallothionein protein SEQ ID No:1.
AC		XX	
AC		KW	Human; metallothionein; heavy metal removal.
XX		XX	
OS		OS	Homo sapiens.
OS	Synthetic.	XX	
OS	/	PN	JP2000060561-A.
XX		XX	
PN	W09854336-A1.	PD	29-FEB-2000.
XX		XX	
PD	03-DEC-1998.	PF	21-AUG-1998; 98JP-0235879.
XX		XX	
PF	28-MAY-1998; 98WO-KR00132.	PR	21-AUG-1998; 98JP-0235879.
XX		XX	
PR	09-APR-1998; 98KR-0013372.	PA	(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PR	28-MAY-1997; 97KR-0021312.	XX	
XX		DR	WPI: 2000-249676/22.
PA	(ROAD) KOREA ADV INST SCI & TECHNOLOGY.	DR	N-PSDB; A08087.
PA	(SAMY-) SAMWANG GENEX CORP.	XX	
XX		PT	New metallothionein polymer used for removal of heavy metals contains
PT		PT	metallothioneins connected together by three amino acid residues -
PT		XX	
XX		PS	Claim 3; Page 8; 19pp; Japanese.
XX		XX	
CC	The present invention describes a metallothionein polymer in which n	CC	
CC	metallothioneins are connected together and the C-terminal amino acid	CC	
CC	residue and the N-terminal amino acid residue of the each adjacent	CC	
CC	metallothionein are combined by three amino acid residues Xaa. The	CC	
DR	WPI: 1999-059844/05.		

CC metallothionein polymer is useful for the removal of heavy metals. The
CC present sequence represents a human metallothionein protein, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 61 AA;

Query Match 100.0%; Score 52; DB 21; Length 61;
Best Local Similarity 20.0%; Pred. No. 2e+02; 0;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXXXCXXXXXXCXXXC 20
|:,:,:,:,:,:,:,:,:,:,:|
Db 29 ckkscccpqgcakcaqg 48

Search completed: March 1, 2001, 16:18:27
Job time: 496 sec